



Appl. No. 09/905,666  
Amdt. Dated April 1, 2004  
Reply to Office Action of October 1, 2003  
Annotated Sheet Showing Changes

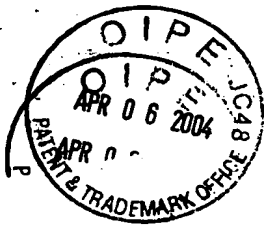
SEQ: 001-405 (pumilus)	(1)	-----ATGAAATTTGTAAGAGGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCAAGTCACATCGC	75
SEQ: 002-406 (subtilis)	(1)	-----ATGAAATTTGTAAGAGGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCTGTTACATCGC	
SEQ: 003-402 (megat.)	(1)	-----ATGAAATTTGTAAGAGGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCAAGTCACATCGC	
SEQ: 004-400 (l. ventus)	(1)	-----ATGAAATTTGTAAGAGGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCAAGTCACATCGC	
SEQ: 005-396 (circul.)	(1)	-----ATGAAATTTGTAAGAGGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCAAGTCACATCGC	
SEQ: 006-392 (azotof.)	(1)	-----ATGAAATTTGTAAGAGGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCAAGTCACATCGC	
SEQ: 007-398 (firmus)	(1)	-----ATGAAATTTGTAAGAGGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCAAGTCACATCGC	
SEQ: 008-393 (badius)	(1)	-----ATGAAATTTGTAAGAGGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCAAGTCACATCGC	
SEQ: 009-395	(1)	-----ATGAAATTTGTAAGAGGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCTGTTACATCGC	
SEQ: 010-396	(1)	-----ATGAAATTTGTAAGAGGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCTGTTACATCGC	
SEQ: 011-397	(1)	-----ATGAAATTTGTAAGAGGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCTGTTACATCGC	
SEQ: 012-398	(1)	-----ATGAAATTTGTAAGAGGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCTGTTACATCGC	
SEQ: 013-399	(1)	-----ATGAAATTTGTAAGAGGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCTGTTACATCGC	
SEQ: 014-400	(1)	-----ATGAAATTTGTAAGAGGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCTGTTACATCGC	
SEQ: 015-401	(1)	-----ATGAAATTTGTAAGAGGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCTGTTACATCGC	
SEQ: 016-402	(1)	-----ATGAAATTTGTAAGAGGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCTGTTACATCGC	
SEQ: 017-403	(1)	-----ATGAAATTTGTAAGAGGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCTGTTACATCGC	
SEQ: 018-404	(1)	-----ATGAAATTTGTAAGAGGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCTGTTACATCGC	
SEQ: 019-405	(1)	-----ATGAAATTTGTAAGAGGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCTGTTACATCGC	
SEQ: 020-406	(1)	-----ATGAAATTTGTAAGAGGAGGATCATTTGCA-----CTTGTAACAAATTTTGGTGCTG-TCTGTTACATCGC	

Delete

Delete

Figure 3a

Figure 3b



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delete

151  
SEQ: 001-405 (pumilus) (139) TCATACAAATTTTGGGGAATTAAAGAGCTATCTCGTATCTCAGGGCTGGTACGGGGCAAGCTGTATGCGGTTGAT  
SEQ: 002-406 (subtilis) (139) TCATTCAATTTTGGGGAATTAAAGAGCTATCTCGTATCTCAGGGCTGGTACGGGGCAAGCTGTATGCGGTTGAT  
SEQ: 003-402 (megat) (139) TCATACAAATTTTGGGGAATTAAAGAGCTATCTCGTATCTCAGGGCTGGTACGGGGCAAGCTGTATGCGGTTGAT  
SEQ: 004-400 (lentus) (139) TCATACAAATTTTGGGGAATTAAAGAGCTATCTCGTATCTCAGGGCTGGTACGGGGCAAGCTGTATGCGGTTGAT  
SEQ: 005-396 (circul) (139) TCATACAAATTTTGGGGAATTAAAGAGCTATCTCGTATCTCAGGGCTGGTACGGGGCAAGCTGTATGCGGTTGAT  
SEQ: 006-392 (azotof) (139) TCATACAAATTTTGGGGAATTAAAGAGCTATCTCGTATCTCAGGGCTGGTACGGGGCAAGCTGTATGCGGTTGAT  
SEQ: 007-398 (firmus) (139) TCATACAAATTTTGGGGAATTAAAGAGCTATCTCGTATCTCAGGGCTGGTACGGGGCAAGCTGTATGCGGTTGAT  
SEQ: 008-393 (badius) (139) TCATACAAATTTTGGGGAATTAAAGAGCTATCTCGTATCTCAGGGCTGGTACGGGGCAAGCTGTATGCGGTTGAT  
SEQ: 009-Dc5h  
SEQ: 010-Dc5f  
SEQ: 011-Dc5c1  
SEQ: 012-Dc5a2  
SEQ: 013-Dc5l2  
SEQ: 014-Sga  
SEQ: 015-Sgc  
SEQ: 016-Sgd  
SEQ: 017-Sgf  
SEQ: 018-Sgh  
SEQ: 019-Mt2b1  
SEQ: 020-H2a  
225

Figure 3c



Appl. No. 09/905,666  
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delete

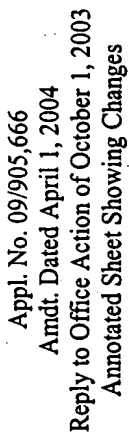
SEQ ID NO.	Sequence	Length
SEQ: 001	405 (pumilus)	(214)
SEQ: 002	406 (subtilis)	(214)
SEQ: 003	402 (megat.)	(214)
SEQ: 004	400 (lentus)	(214)
SEQ: 005	396 (clixcul.)	(214)
SEQ: 006	392 (azobof.)	(214)
SEQ: 007	398 (firmus)	(214)
SEQ: 008	393 (badius)	(214)
SEQ: 009	109 (dc5h)	(214)
SEQ: 010	110 (dc5h)	(214)
SEQ: 011	111 (dc5c1)	(223)
SEQ: 012	112 (dc5a2)	(223)
SEQ: 013	113 (dc5l2)	(223)
SEQ: 014	114 (sga)	(214)
SEQ: 015	115 (sgc)	(214)
SEQ: 016	116 (sgd)	(214)
SEQ: 017	117 (sgf)	(214)
SEQ: 018	118 (sgn)	(214)
SEQ: 019	119 (mt2b1)	(223)
SEQ: 020	120 (h2a)	(214)

226

TTTTGGGACAAAGACAGGGACGGAATTATAACAATGGCCCGGTATTATCACGATTTGTGCAAAAGGTTTTAGACGAA  
TTTTGGGACAAAGACAGGGACGGAATTATAACAATGGCCCGGTATTATCACGATTTGTGCAAAAGGTTTTAGATGAA  
TTTTGGGACAAAGACAGGGACGGAATTATAACAATGGCCCGGTATTATCACGATTTGTGCAAAAGGTTTTAGACGAA  
TTTTGGGACAAAGACAGGGACGGAATTATAACAATGGCCCGGTATTATCACGATTTGTGCAAAAGGTTTTAGACGAA  
TTTTGGGACAAAGACAGGGACGGAATTATAACAATGGCCCGGTATTATCACGATTTGTGCAAAAGGTTTTAGACGAA  
TTTTGGGACAAAGACAGGGACGGAATTATAACAATGGCCCGGTATTATCACGATTTGTGCAAAAGGTTTTAGACGAA  
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TTCAGGGACAAAGACAGGGACGGAATTATAACAATGGCCCGGTATTATCACGATTTGTGCAAAAGGTTTTAGACAAA

300

Figure 3d



301

SEQ: 001-405 (pumilus)	(289)	ACGGGTGCGAAAAAAGTGGAATATTGTCGCTCACAGTATGGGTGGCGCGAACAACACACACCTTACTACATAAAAAAATCTG
SEQ: 002-406 (subtilis)	(289)	ACGGGTGCGAAAAAAGTGGAATATTGTCGCTCACAGCATGGGGGGCGCGAACAACACACTTTTACTACATAAAAAAATCTG
SEQ: 003-407 (megat.)	(289)	ACGGGTGCGAAAAAAGTGGAATATTGTCGCTCACAGCATGGGTGGCGCGAACAACACACTTTTACTACATAAAAAAATCTG
SEQ: 004-408 (lentus)	(289)	ACGGGTGCGAAAAAAGTGGAATATTGTCGCTCACAGCATGGGTGGCGCGAACAACACACTTTTACTACATAAAAAAATCTG
SEQ: 005-409 (circul.)	(289)	ACGGGTGCGAAAAAAGTGGAATATTGTCGCTCACAGCATGGGTGGCGCGAACAACACACTTTTACTACATAAAAAAATCTG
SEQ: 006-410 (azotof.)	(289)	ACGGGTGCGAAAAAAGTGGAATATTGTCGCTCACAGCATGGGTGGCGCGAACAACACACTTTTACTACATAAAAAAATCTG
SEQ: 007-411 (firmus)	(289)	ACGGGTGCGAAAAAAGTGGAATATTGTCGCTCACAGCATGGGTGGCGCGAACAACACACTTTTACTACATAAAAAAATCTG
SEQ: 008-412 (badius)	(289)	ACGGGTGCGAAAAAAGTGGAATATTGTCGCTCACAGCATGGGTGGCGCGAACAACACACTTTTACTACATAAAAAAATCTG
SEQ: 009-413 (Dc5h)	(289)	ACGGGTGCGAAAAAAGTGGAATATTGTCGCTCACAGCATGGGTGGCGCGAACAACACACTTTTACTACATAAAAAAATCTG
SEQ: 010-414 (Dc5f)	(289)	ACGGGTGCGAAAAAAGTGGAATATTGTCGCTCACAGCATGGGTGGCGCGAACAACACACTTTTACTACATAAAAAAATCTG
SEQ: 011-415 (Dc5c1)	(298)	ACGGGTGCGAAAAAAGTGGAATATTGTCGCTCACAGTATGGGTGGAGCGAACAACACGCTATATCAAGAATCTA
SEQ: 012-416 (Dc5a2)	(298)	ACAGGTGCGAAAAAAGTGGAATATTGTCGCTCATAGTATGGGTGGGTGCGAACAACACGTTATATATAAAAAACCTA
SEQ: 013-417 (Dc512)	(298)	ACGGGTGCGAAAAAAGTGGAATATTGTCGCTCATAGTATGGGTGGAGCGAACAACACGTTATATATAAGAATCTA
SEQ: 014-418 (Sga)	(289)	ACGGGTGCGAAAAAAGTGGAATATTGTCGCTCACAGCATGGGTGGCGCGCTAACACGCTTTTACTACATAAAAAAATTTG
SEQ: 015-419 (Sgc)	(289)	ACGGGTGCGAAAAAAGTGGAATATTGTCGCTCACAGCATGGGTGGCGCGCTAACACGCTTTTACTACATAAAAAAATTTG
SEQ: 016-420 (Sgd)	(289)	ACGGGTGCGAAAAAAGTGGAATATTGTCGCTCACAGCATGGGTGGCGCGCTAACACGCTTTTACTACATAAAAAAATTTG
SEQ: 017-421 (Sgf)	(289)	ACAGGAGCCAAAAAAGTAGAATATTGTCGCTCATAGTATGGGTGGAGCGAACAACACTTATATTAAGAATCTA
SEQ: 018-422 (Sgi)	(289)	ACAGGAGCCAAAAAAGTAGAATATTGTCGCTCATAGTATGGGTGGAGCGAACAACACTTATATTAAGAATCTA
SEQ: 019-423 (Mt2b1)	(298)	ACGGGTGCGAAAAAAGTAGAATATTGTCGCGCATAGTATGGGTGGCGAACAACACGCTATATTAAGAATCTA
SEQ: 020-424 (H2a)	(289)	ACGGGTGCGAAAAAAGTAGAATATTGTCGCTCATAGTATGGGTGGCGAACAACACGCTATATTAAGAATCTA

Figure 3e



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20/20

376 450

SEQ:0011406 (pumilus) (364) GACGGCGGAAATAAAATTGAAAACGTCGTAAACGCTTGGCGGGCGGAACCGTTGACGACAAAGCAAGCGCTTCCG  
SEQ:002406 (subtilis) (364) GACGGCGGAAATAAAAGTTGCAACGTCGTGACGCTTGGCGGGCGGAACCGTTGACGACAGGCAAGCGCTTCCG  
SEQ:003402 (megat.) (364) GACGGCGGAAATAAAATTGAAAACGTCGTAAACGCTTGGCGGGCGGAACCGTTGACGACAAAGCAAGCGCTTCCG  
SEQ:004400 (lentus) (364) GACGGCGGAAATAAAATTGAAAACGTCGTAAACGCTTGGCGGGCGGAACCGTTGACGACAAAGCAAGCGCTTCCG  
SEQ:005396 (circul.) (364) GACGGCGGAAATAAAATTGAAAACGTCGTAAACGCTTGGCGGGCGGAACCGTTGACGACAAAGCAAGCGCTTCCG  
SEQ:006392 (azotof.) (364) GACGGCGGAAATAAAATTGAAAACGTCGTAAACGCTTGGCGGGCGGAACCGTTGACGACAAAGCAAGCGCTTCCG  
SEQ:007398 (firmus) (364) GACGGCGGAAATAAAATTGAAAACGTCGTAAACGCTTGGCGGGCGGAACCGTTGACGACAAAGCAAGCGCTTCCG  
SEQ:008393 (badius) (364) GACGGCGGAAATAAAATTGAAAACGTCGTAAACGCTTGGCGGGCGGAACCGTTGACGACAAAGCAAGCGCTTCCG  
SEQ:009-Dc5h (364) GACGGCGGAAATAAAATTGAAAACGTCGTAAACGCTTGGCGGGCGGAACCGTTGACGACAAAGCAAGCGCTTCCG  
SEQ:010-Dc5f (364) GATGGCGGCGATATAAAATTGAAAACGTCGTAAACGCTTGGCGGGCGGAACCGTTGACGACAAAGCAAGCGCTTCCG  
SEQ:011-Dc5c1 (373) GACGGTGGAGATATAAAATTGAAAACGTCGTAAACGCTTGGCGGGCGGAACCGTTGACGACAAAGCAAGCGCTTCCG  
SEQ:012-Dc5a2 (373) GACGGCGGCGATATAAAATTGAAAACGTCGTAAACGCTTGGCGGGCGGAACCGTTGACGACAAAGCAAGCGCTTCCG  
SEQ:013-Dc512 (373) GATGGCGGCGATATAAAATTGAAAACGTCGTAAACGCTTGGCGGGCGGAACCGTTGACGACAAAGCAAGCGCTTCCG  
SEQ:014-Sga (364) GATGGCGGTAATAAAATTGAAAACGTCGTAAACGCTTGGCGGGCGGAACCGTTGACGACAAAGCAAGCGCTTCCG  
SEQ:015-Sgc (364) GATGGCGGTAATAAAATTGAAAACGTCGTAAACGCTTGGCGGGCGGAACCGTTGACGACAAAGCAAGCGCTTCCG  
SEQ:016-Sgd (364) GATGGCGGTAATAAAATTGAAAACGTCGTAAACGCTTGGCGGGCGGAACCGTTGACGACAAAGCAAGCGCTTCCG  
SEQ:017-Sgf (364) GATGGTGGCGATATAAAATTGAAAACGTCGTAAACGCTTGGCGGGCGGAACCGTTGACGACAAAGCAAGCGCTTCCG  
SEQ:018-Sgn (364) GATGGTGGCGATATAAAATTGAAAACGTCGTAAACGCTTGGCGGGCGGAACCGTTGACGACAAAGCAAGCGCTTCCG  
SEQ:019-Mt2b1 (373) GATGGCGGCGATATAAAATTGAAAACGTCGTAAACGCTTGGCGGGCGGAACCGTTGACGACAAAGCAAGCGCTTCCG  
SEQ:020-H2a (364) GATGGCGGCGATATAAAATTGAAAACGTCGTAAACGCTTGGCGGGCGGAACCGTTGACGACAAAGCAAGCGCTTCCG

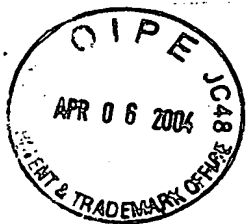
Figure 3f

525

451

SEQ:001-405 (pumilus) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATGATGATGTCATGAATTACTT  
SEQ:002-406 (subtilis) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATGATGATGTCATGAATTACTT  
SEQ:003-402 (negat.) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATGATGATGTCATGAATTACTT  
SEQ:004-400 (lentos) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATGATGATGTCATGAATTACTT  
SEQ:005-396 (circul.) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATGATGATGTCATGAATTACTT  
SEQ:006-392 (azotof.) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATGATGATGTCATGAATTACTT  
SEQ:007-398 (firmus) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATGATGATGTCATGAATTACTT  
SEQ:008-393 (badius) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTACACATGATGATGTCATGAATTACTT  
SEQ:009-Dc5h (439) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCGTCCTATA-GCTCAGCAGATCTTATTGTCGTCACACAGCCT  
SEQ:010-Dc5f (439) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCGTCCTATA-GCTCAGCAGATCTTATTGTCGTCACACAGCCT  
SEQ:011-Dc5c1 (448) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCGTCCTATA-GCTCAGCAGATCTTATTGTCGTCACACAGCCT  
SEQ:012-Dc5a2 (448) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCGTCCTATA-GCTCAGCAGATCTTATTGTCGTCACACAGCCT  
SEQ:013-Dc512 (448) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCGTCCTATA-GCTCAGCAGATCTTATTGTCGTCACACAGCCT  
SEQ:014-Sga (439) GGTACTGATCCCAACCAAAAAGATTTGTCACACATCCGTCCTATA-GTACTGCTGATATGATGTTGTTATGAATTACTT  
SEQ:015-Sgc (439) GGTACTGATCCCAACCAAAAAGATTTGTCACACATCCGTCCTATA-GTACTGCTGATATGATGTTGTTATGAATTACTT  
SEQ:016-Sgd (439) GGTACTGATCCCAACCAAAAAGATTTGTCACACATCCGTCCTATA-GTACTGCTGATATGATGTTGTTATGAATTACTT  
SEQ:017-Sgf (439) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCGTCCTATA-GCTCAGCAGATCTTATTGTCGTCACACAGCCT  
SEQ:018-Sgh (439) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCGTCCTATA-GCTCAGCAGATCTTATTGTCGTCACACAGCCT  
SEQ:019-Mt2b1 (448) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCGTCCTATA-GCTCAGCAGATTTGATGTTGTCGTCACACAGCCT  
SEQ:020-H2a (439) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCGTCCTACAAGCTCAGCCGATCTCATTTGTCGTCACACAGCCT

Figure 39



Appl. No. 09/905,666  
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Delete

SEQ:001-405 (pumilus)	(513)	ATCAAAATTAGACGGT-GCTAAAAAC-GCTCAAAATTCATGGCGTTGGGCACACATTGGTTTATTGATGAACAGCCAA	600
SEQ:002-408 (subtilis)	(513)	ATCAAGATTAGATGGT-GCTAGAAAC-GTTCAAAATCCATGGCGTTGGACACATCGGCCCTTCTGTACAGCAGCCAA	
SEQ:003-402 (megat.)	(513)	ATCAAAATTAGACGGT-GCTAAAAAC-GTTCAAAATTCATGGCGTTGGGCACACATTGGTTTATTGATGAACAGCCAA	
SEQ:004-400 (lentus)	(513)	ATCAAAATTAGACGGT-GCTAAAAAC-GTTCAAAATTCATGGCGTTGGGCACACATTGGTTTATTGATGAACAGCCAA	
SEQ:005-396 (cilicul.)	(513)	ATCAAAATTAGACGGT-GCTAAAAAC-GTTCAAAATTCATGGCGTTGGGCACACATTGGTTTATTGATGAACAGCCAA	
SEQ:006-392 (azotof.)	(513)	ATCAAAATTAGACGGT-GCTAAAAAC-GTTCAAAATTCATGGCGTTGGGCACACATTGGTTTATTGATGAACAGCCAA	
SEQ:007-398 (firmus)	(513)	ATCAAAATTAGACGGT-GCTAAAAAC-GTTCAAAATTCATGGCGTTGGGCACACATTGGTTTATTGATGAACAGCCAA	
SEQ:008-393 (badius)	(513)	ATCAAAATTAGACGGT-GCTAAAAAC-GTTCAAAATTCATGGCGTTGGGCACACATTGGTTTATTGATGAACAGCCAA	
SEQ:009-Dc51a	(513)	ATCAAGATTAGATGGT-GCGAGAAAC-GTTCAAAATCCATGGCGTTGGGCACACATCGGCCCTTCTGTACAGCAGCCAA	
SEQ:010-Dc5f	(513)	CTCTCGTTTAAATTGGC-GCAAGAAAC-ATCCTGATCCATGGCGTTGGTCATATCGGTCTATTAACTCAAGCCAA	
SEQ:011-Dc5c1	(522)	TTTCGC-GTTTAAATTGGCGCAAGAAAC-GTCTGATCCACGGCGTTGGACATATCGGTCTATTAACTCAAGCCAA	
SEQ:012-Dc5a2	(522)	CTCGC-GTTTAAATTGGCGCAAGAAAC-GTCTCAATTCACGGCGTTGGTCACATCGGTCTATTAGTTCAAGCCAA	
SEQ:013-Dc512	(522)	CTCTCAGTTTAAATTGGCGCAAGAAAC-ATCCTGATCCA-GGCGTTGGTCATATCGGTCTATTAACTCAAGCCAA	
SEQ:014-Sga	(513)	AACAAATTAGACGGG-GCTAAAAAT-GTTCAAAATTCATGGTGTGGACATATCGGCCCTTCTGTACAGCAGCCAA	
SEQ:015-Sgc	(513)	ATCAAAATTAGACGGG-GCTAAAAAT-GTTCAAAATTCATGGTGTGGACATATCGGCCCTTCTGTACAGCAGCCAA	
SEQ:016-Sga	(513)	ATCAAAATTAGACGGG-GCTAAAAAT-GTTCAAAATTCATGGTGTGGACATATCGGCCCTTCTGTACAGCAGCCAA	
SEQ:017-Sgf	(513)	CTCTCGTTTAAATTGGC-GCAAGAAAC-GTCCAAATCCATGGCGTTGGACATATCGGTCTATTAACTCAAGCCAA	
SEQ:018-Sgh	(513)	CTCTCGTTTAAATTGGC-GCAAGAAAC-GTCCAAATCCATGGCGTTGGACATATCGGTCTATTAACTCAAGCCAA	
SEQ:019-Mt2b1	(522)	TTTCGC-GTTTAACTGGCGCAAGAAAT-GTCTGATCCACGGCGTTGGCCATATCGGTCTATTAACTCAAGCCAA	
SEQ:020-H2a	(514)	CTCTCGTTTAAATTGGCTGCAAGAAACAGTCCAAATCCATGGCGTTGGACATATCGGTCTATTAACTCAAGCCAA	

Figure 3h





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SEQ: 001-405 (pumilus)	(586)	GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGCCAAAATACGAATTAA	601	654
SEQ: 002-406 (subtilis)	(586)	GTCAACAGCCTGATTAAAGAGGCTGAACGGCGGGGGCTCAATACAAATTAG		
SEQ: 003-402 (megat.)	(586)	GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGCCACAATACAAATTAA		
SEQ: 004-400 (tentus)	(586)	GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGCTAAATACAAATTAA		
SEQ: 005-396 (circul.)	(586)	GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGCTCAATACAAATTAA		
SEQ: 006-392 (azobof.)	(586)	GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGCTTAGATACAAATTAA		
SEQ: 007-398 (firmus)	(586)	GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGCCACAATACAAATTAA		
SEQ: 008-393 (badius)	(586)	GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGCCACAATACAAATTAA		
SEQ: 009-Dc50	(586)	GTCAACAGCCTGATTAAAGAGGCTGAACGGCGGGGGCTCAATACAAATTAA		
SEQ: 010-Dc51	(586)	GTGAAAGGCTATATTAAAGAGGACTGAACGGCGGGGGCTCAATACAAATTAA		
SEQ: 011-Dc5c1	(595)	GTCAAGGCTATGTGAAAGAGGATTTGAATGGCGGGGGACAGAAATACAAATTAA		
SEQ: 012-Dc5a2	(595)	GTCAAGGCTATATCAAGAGGACTGAATGGCGGGGGCCAAAATACAAATTAA		
SEQ: 013-Dc512	(595)	GTGAAAGGCTATATTAAAGAGGACTGAACGGCGGGGGCTCAATACAAATTAA		
SEQ: 014-Sga	(586)	GTCAACAGCCTGATTAAAGAGGCTTAACGGCGGGGGCTCAATACAAATTAA		
SEQ: 015-Sgc	(586)	GTCAATAGCCTGATTAAAGAGGCTTAACGGCGGGGGCTCAATACGAATTAA		
SEQ: 016-Sgd	(586)	GTCAACAGCCTGATTAAAGAGGCTTAACGGCGGGGGCTGAATACGAATTAA		
SEQ: 017-Sgf	(586)	GTCAAGGATATATTAAAGAGGACTGAACGGCGGGGGCTCAATACAAATTAA		
SEQ: 018-Sgh	(586)	GTCAAGGATATATTAAAGAGGACTGAACGGCGGGGGCCAAAATACAAATTAA		
SEQ: 019-Mt2b1	(595)	GTGAAAGGCTATATTAAAGAGGACTGAACGGCGGGGGCTAAATACAAATTAA		
SEQ: 020-H2a	(589)	GTCAAGGATATATTAAAGAGGACTGAACGGCGGGGGCTAAATACAAATTAA		

Figure 3i

SEQ: 021-1f15 (G2)  
 SEQ: 022-3C12  
 SEQ: 023-3N19 (G2)  
 SEQ: 024-G2.2  
 SEQ: 025-2B3  
 SEQ: 026-2F11  
 SEQ: 027-KV1 (6C7)  
 SEQ: 028-KV6 (3A1)  
 SEQ: 029-KV2 (2D1)  
 SEQ: 030-N2.5  
 SEQ: 031-KV5 (2H6)  
 SEQ: 032-3B5  
 SEQ: 033-G2.1  
 SEQ: 034-3H24 (G2)  
 SEQ: 035-KV10 (4G6)  
 SEQ: 036-KV12 (6D4)  
 SEQ: 037-N2.2  
 SEQ: 038-N2.3  
 SEQ: 039-N2.1  
 SEQ: 040-KV4 (2E12)  
 SEQ: 041-KV9 (4C6)  
 SEQ: 042-7D6  
 SEQ: 043-3F3  
 SEQ: 044-2D11 (G2)  
 SEQ: 045-3C23 (G2)  
 SEQ: 046-G2.3  
 SEQ: 047-2A3  
 SEQ: 048-2F4  
 SEQ: 049-2B9 (G2)  
 SEQ: 050-2C5  
 SEQ: 051-KV1 (2A6)  
 SEQ: 052-2D12 (G2)  
 SEQ: 053-3C8  
 SEQ: 054-2D5

Figure 4a



Appl. No. 09/905,666  
Amdt. Dated April 1, 2004  
Reply to Office Action of October 1, 2003  
Annotated Sheet Showing Changes

Dele

76 150

SEQ: 021-1E15 (G2)	(76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 022-3C12	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 023-3N19 (G2)	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 024-2G2.2	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 025-2C3	(76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 026-2F11	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 027-KV11 (6C7)	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 028-KV6 (3A1)	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 029-KV2 (2D1)	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 030-N2.5	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 031-KV5 (2H6)	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 032-3E5	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 033-G2.1	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 034-3H24 (G2)	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 035-KV10 (4G6)	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 036-KV12 (6D4)	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 037-N2.2	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 038-N2.3	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 039-N2.1	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 040-KV4 (2E12)	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 041-KV9 (4C6)	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 042-7D6	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 043-3F3	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 044-2D11 (G2)	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 045-3C23 (G2)	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 046-G2.3	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 047-2A3	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 048-2F4	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 049-2B9 (G2)	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 050-2C5	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 051-KV1 (2A6)	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 052-2D13 (G2)	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 053-3C8	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA
SEQ: 054-2D5	(76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGGAATTATAACAA

Figure 4b



Appl. No. 09/905,666  
Amdt. Dated April 1, 2004  
Reply to Office Action of October 1, 2003  
Annotated Sheet Showing Changes

delete

151 225

SEQ: 021-1f15 (G2) (151) TGGCCCGGTATTATCGCGTTTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 022-3C12 (151) TGGCCCGGTATTATCTAGATTCGTCAAGATGTCTAGACAAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 023-3N19 (G2) (151) TGGCCCGGTATTATCACGATTGTGAAAAAGGTAATTAGATGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 024-22.2 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 025-2C3 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 026-2F11 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 027-KV11 (6C7) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 028-KV6 (3A1) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 029-KV2 (2D1) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 030-N2.5 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 031-KV5 (2H6) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 032-3E5 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 033-G2.1 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 034-3H24 (G2) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 035-KV10 (4G6) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 036-KV12 (6D4) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 037-N2.2 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 038-N2.3 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 039-N2.1 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 040-KV4 (2E12) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 041-KV9 (4C6) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 042-7D6 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 043-3E2 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 044-2D11 (G2) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 045-3C23 (G2) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 046-G2.3 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 047-2A3 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 048-2F4 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 049-2B9 (G2) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 050-2C5 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 051-KV1 (2A6) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 052-2D13 (G2) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 053-3C8 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

SEQ: 054-2D5 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTGCGCTCA

Figure 4c



Appl. No. 09/905,666  
Amdt. Dated April 1, 2004  
Reply to Office Action of October 1, 2003  
Annotated Sheet Showing Changes

226  
SEQ: 021-1F15 (G2) (226) CAGCATGGGGGGCGCTAACACGCTTTACTACATAAAAAATCTGGACGGCGGAAATAAAGTTGAAAAACGTCGTAAC  
SEQ: 022-3C12 (226) CAGCATGGGGGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 023-3N19 (G2) (226) CAGCATGGGTGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 024-G2.2 (226) CAGCATGGGGGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 025-2C3 (226) CAGCATGGGGGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 026-2F11 (226) CAGCATGGGTGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 027-KV11 (6C7) (226) CAGTATGGTGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 028-KV6 (3A1) (226) CAGTATGGTGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 029-KV2 (2D1) (226) CAGCATGGGTGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 030-N2.5 (226) CAGCATGGGGGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 031-KV5 (2H6) (226) CAGCATGGGTGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 032-3E5 (226) CAGCATGGGTGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 033-G2.1 (226) CAGCATGGGGGGCGTAACACGCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 034-3H24 (G2) (226) CAGCATGGGGGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 035-KV10 (4C6) (226) CAGCATGGGTGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 036-KV12 (6D4) (226) CAGCATGGGTGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 037-N2.2 (226) CAGCATGGGTGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 038-N2.3 (226) CAGCATGGGTGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 039-N2.1 (226) CAGCATGGGTGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 040-KV4 (2E12) (226) CAGCATGGGGGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 041-KV9 (4C6) (226) CAGCATGGGGGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 042-7D6 (226) CAGCATGGGTGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 043-3F3 (226) CAGCATGGGTGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 044-2D11 (G2) (226) CAGCATGGGGGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 045-3C23 (G2) (226) CAGCATGGGGGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 046-G2.3 (226) CAGCATGGGTGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 047-2A3 (226) CAGCATGGGGGGCGTAACACGCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 048-2F4 (226) CAGCATGGGTGGCGTAACACGCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 049-2B9 (G2) (226) CAGCATGGGGGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 050-2C5 (226) CAGCATGGGTGGCGTAACACGCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 051-KV1 (2A6) (226) CAGCATGGGGGGCGTAACACGCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 052-2D13 (G2) (226) CAGCATGGGTGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 053-3C8 (226) CAGCATGGGTGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC  
SEQ: 054-2D5 (226) CAGCATGGGTGGCGGAACACACCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATTTGAAAAACGTCGTAAC

Figure 4d

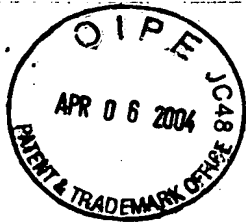


Appl. No. 09/905,666  
Amdt. Dated April 1, 2004  
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Annotated Sheet Showing Changes

SEQ: 021-1N15 (G2)	(301)	GC	TTGGCGGCACGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC	301	375
SEQ: 022-3C12	(301)	GC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 023-3N19 (G2)	(301)	GC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 024-G2.2	(301)	GC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 025-2C3	(301)	CA	TTGGTAGAGCAACCGGACTCGTTTCAAGCAGAGATTTACAGGCACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 026-2F11	(301)	GC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 027-FR1A (6C7)	(301)	GC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 028-KV6 (3A1)	(301)	GC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 029-KV2 (2D1)	(301)	GC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 030-N2.5	(301)	GC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 031-KV5 (2H6)	(301)	GC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 032-3E5	(301)	GC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 033-2.1	(301)	GC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 034-3H24 (G2)	(301)	GC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 035-KV10 (4G6)	(301)	AC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 036-KV12 (6D4)	(301)	GC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 037-N2.2	(301)	GC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 038-N2.3	(301)	GC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 039-N2.1	(301)	GC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 040-KV4 (2E12)	(301)	GC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 041-KV9 (4C6)	(301)	AC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 042-7D6	(301)	AC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 043-3F3	(301)	GC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 044-2D11 (G2)	(301)	AC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 045-3C23 (G2)	(301)	AC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 046-G2.3	(301)	GC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 047-2A3	(301)	GC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 048-2F4	(301)	AC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 049-2B9 (G2)	(301)	AC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 050-2C5	(301)	AC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 051-KV1 (2A6)	(301)	GC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 052-2D13 (G2)	(301)	GC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 053-3C8	(301)	AC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		
SEQ: 054-2D5	(301)	AC	TTGGCGGCAGAACCGGTCGACACAAGCAAGGCGCTCCGGGAACAGATCCAAATCAAAAGATTTTATACAC		

Figure 4e





Appl. No. 09/905,666  
Amdt. Dated April 1, 2004  
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Annotated Sheet Showing Changes

525

451

SEQ: 021-1f15 (G2) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 022-3C22 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 023-3N19 (G2) (451) CCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 024-G2.2 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 025-2C3 (451) CCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 026-2F41 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 027-KV11 (6Z7) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 028-KV6 (2A1) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 029-KV2 (2D1) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 030-N2.5 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 031-KV5 (2H6) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 032-3E5 (451) CCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 033-G2.1 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 034-3H24 (G2) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 035-KV10 (4G6) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 036-KV12 (6P4) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 037-N2.2 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 038-N2.3 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 039-N2.1 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 040-KV4 (2E2) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 041-KV9 (4C6) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 042-7D6 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 043-3F3 (451) CCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 044-2D11 (G2) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 045-3C23 (G2) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 046-G2.3 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 047-2A3 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 048-2F4 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 049-2B9 (G2) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 050-2G5 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 051-KV1 (2A6) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 052-2D13 (G2) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 053-3C8 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

SEQ: 054-2D5 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAACTCAACAGCCTGATTTAAAGAGGACTGAACCGCGG

Figure 49





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Annotated Sheet Showing Changes

*delete*

	526	544
SEQ: 021-1f15 (G2)	(526)	GGGACTCAATACGAATTGA
SEQ: 022-3012	(526)	GGGACTCAATACGAATTGA
SEQ: 023-3N19 (G2)	(526)	GGGACTGAATACAAAATTGA
SEQ: 024-G2.2	(526)	GGGACTCAATACGAATTGA
SEQ: 025-2C3	(526)	GGGCCACAATACGAATTGA
SEQ: 026-2F11	(526)	AGGCTAAATACGAATTGA
SEQ: 027-KV11 (6C7)	(526)	GGGCTAAATACAAAATTGA
SEQ: 028-KV6 (3A1)	(526)	GGGCTAAATACAAAATTGA
SEQ: 029-KV2 (2D1)	(526)	GGGCCAAAATACAAAATTGA
SEQ: 030-N2.5	(526)	GGGCCACAATACAAAATTGA
SEQ: 031-KV5 (2H6)	(526)	GGGCTGAATACAAAATTGA
SEQ: 032-3E5	(526)	GGGCTCAATACGAATTGA
SEQ: 033-G2.1	(526)	GGGACTCAATACGAATTGA
SEQ: 034-3H24 (G2)	(526)	GGGACTCAATACGAATTGA
SEQ: 035-KV10 (4G6)	(526)	GGGCCACAATACAAAATTGA
SEQ: 036-KV12 (6D4)	(526)	AGGCCACAATACAAAATTGA
SEQ: 037-N2.2	(526)	AGGCCACAATACAAAATTGA
SEQ: 038-N2.3	(526)	AGGCCACAATACAAAATTGA
SEQ: 039-N2.1	(526)	AGGCCACAATACAAAATTGA
SEQ: 040-KV4 (2E12)	(526)	GGGCCACAATACAAAATTGA
SEQ: 041-KV9 (4C6)	(526)	GGGCCACAATACGAATTGA
SEQ: 042-7D6	(526)	GGGATTAATACGAATTGA
SEQ: 043-3F3	(526)	GGGCCAGAATACGAATTGA
SEQ: 044-2D11 (G2)	(526)	AGGCCAGAATACGAATTGA
SEQ: 045-3C23 (G2)	(526)	GGGCCACAATACGAATTGA
SEQ: 046-G2.3	(526)	GGGCCAGAATACGAATTGA
SEQ: 047-2A3	(526)	AGGCTAAATACAAAATTGA
SEQ: 048-2F4	(526)	AGGCCAGAATACGAATTGA
SEQ: 049-2B9 (G2)	(526)	AGGCCAAAATACGAATTGA
SEQ: 050-2C5	(526)	AGGCCAAAATACGAATTGA
SEQ: 051-KV1 (2A6)	(526)	GGGCCAGAATACGAATTGA
SEQ: 052-2D13 (G2)	(526)	AGGCCAAAATACGAATTGA
SEQ: 053-3C8	(526)	GGGCCAAAATACAAAATTGA
SEQ: 054-2D5	(526)	AGGACAAAATACAAAATTGA

Figure 4h



SEQ: 0551-405 (pumilus)	(1)	--MKFVKRRRIIALVTILVLSVTSLFAMQP-SAKAA	(Signal peptide)	(Mature region)	40
SEQ: 0561-406 (subtilis)	(1)	--MKFVKRRRIIALVTILVLSVTSLFALQP-SAKAA			
SEQ: 057-402 (negat.)	(1)	--MKFVKRRRIIALVTILVLSVTSLFAMQP-SAKAA			
SEQ: 058-400 (lentus)	(1)	--MKFVKRRRIIALVTILVLSVTSLFAMQP-SAKAA			
SEQ: 059-396 (circul.)	(1)	--MKFVKRRRIIALVTILVLSVTSLFAMQP-SAKAA			
SEQ: 060-392 (azotox.)	(1)	--MKFVKRRRIIALVTILVLSVTSLFAMQP-SAKAA			
SEQ: 061-398 (firmus)	(1)	--MKFVKRRRIIALVTILVLSVTSLFAMQP-SAKAA			
SEQ: 062-393 (badius)	(1)	--MKFVKRRRIIALVTILVLSVTSLFAMQP-SAKAA			
SEQ: 063-Dc5h	(1)	--MKFVKRRRIIALVTILVLSVTSLFALQP-SAKAA			
SEQ: 064-Dc5f	(1)	--MKFVKRRRIIALVTILVLSVTSLFALQP-SAKAA			
SEQ: 065-Dc5c1	(1)	--MKFVKRRRIIALVTILVLSVTSLFALQP-SAKAA			
SEQ: 066-Dc5a2	(1)	--MKFVKRRRIIALVTILVLSVTSLFALQP-SAKAA			
SEQ: 067-Dc512	(1)	--MKFVKRRRIIALVTILVLSVTSLFALQP-SAKAA			
SEQ: 068-Sga	(1)	--MKFVKRRRIIALVTILVLSVTSLFALQP-SAKAA			
SEQ: 069-Sgc	(1)	--MKFVKRRRIIALVTILVLSVTSLFALQP-SAKAA			
SEQ: 070-Sgd	(1)	--MKFVKRRRIIALVTILVLSVTSLFALQP-SAKAA			
SEQ: 071-Sgf	(1)	--MKFVKRRRIIALVTILVLSVTSLFALQP-SAKAA			
SEQ: 072-Sgh	(1)	--MKFVKRRRIIALVTILVLSVTSLFALQP-SAKAA			
SEQ: 073-Mt2b1	(1)	--MKFVKRRRIIALVTILVLSVTSLFALQP-SAKAA			
SEQ: 074-H2a	(1)	--MKFVKRRRIIALVTILVLSVTSLFALQP-SAKAA			

Figure 5a

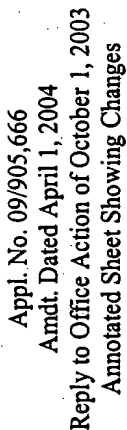


Figure 5b

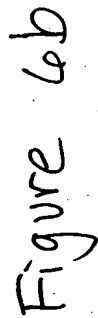


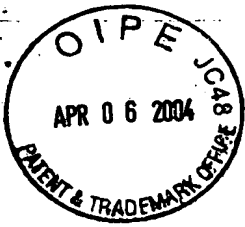
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Figure 5c







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	151	180
SEQ: 075-1F15 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 076-3C12	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 077-3N19 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 078-G2.2	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 079-2C3	(151)	HGVGHIGLLTSSQVKGVIKEGLNGGGLNTN
SEQ: 080-2F11	(151)	HGVGHIGLLMNSQVKGVIKEGLNGGGLNTN
SEQ: 081-KV11 (6C7)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 082-KV8 (3A1)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 083-KV2 (2D1)	(151)	HGVGHIGLLYSSQVNSLIKEGLNGGGLNTN
SEQ: 084-N2.5	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 085-KV5 (2H6)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 086-3E5	(151)	HGVGHIGLLYSSQVNSLIKEGLNGGGLNTN
SEQ: 087-G2.1	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 088-3H24 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 089-KV10 (4G6)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 090-KV12 (6D4)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 091-N2.2	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 092-N2.3	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 093-N2.1	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 094-KV4 (2E12)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 095-KV9 (4C6)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 096-YD6	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 097-3R3	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 098-2D11 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 099-3C23 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 100-G2.3	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 101-2A1	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 102-2F4	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 103-2B9 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 104-2E5	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 105-KV11 (2A6)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 106-2D13 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 107-3E8	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 108-2D5	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN

Figure 6c



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SEQ: 001	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCAGTCACATCGC
SEQ: 002	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCTGTTACATCGC
SEQ: 003	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCAGTCACATCGC
SEQ: 004	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCAGTCACATCGC
SEQ: 005	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCAGTCACATCGC
SEQ: 006	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCAGTCACATCGC
SEQ: 007	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCAGTCACATCGC
SEQ: 008	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCAGTCACATCGC
SEQ: 009	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCAGTCACATCGC
SEQ: 010	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCTGTTACATCGC
SEQ: 011	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCTGTTACATCGC
SEQ: 012	(1)	ATGAAAGTGATTTTGTAAAGAAAAGGAGT-TTGCAAAATTCCTTGTGCCCCCTTGCCCTTAGTGCTAGGTTCAATAGC
SEQ: 013	(1)	ATGAAAGTGATTTTGTAAAGAAAAGGAGT-TTGCAAAATTCCTTGTGCCCCCTTGCCCTTAGTGCTAGGTTCAATAGC
SEQ: 014	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCTGTTACATCGC
SEQ: 015	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCTGTTACATCGC
SEQ: 016	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCTGTTACATCGC
SEQ: 017	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCTGTTACATCGC
SEQ: 018	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCTGTTACATCGC
SEQ: 019	(1)	ATGAAAGTGATTTTGTAAAGAAAAGGAGT-TTGCAAAATTCCTTGTGCCCCCTTGCCCTTAGTGCTAGGTTCAATAGC
SEQ: 020	(1)	-----ATGAAATTTGTAAAAAGAGGATCATTTGCA-----CTTGTAAACAATTTGGTGCTG-TCTGTTACATCGC

FIGURE 3a





		(Signal peptide coding region)	(Mature coding region)
SEQ: 001	76	TGTTTGGGATGCGAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 002	(65)	TGTTTGGGATGCGAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 003	(65)	TGTTTGGGATGCGAGCCGTCAGCAAAAGCCGCT	GA-CACAATCCAGTTGTTATGTTTCACACTGGTATCGGAGGAGCT
SEQ: 004	(65)	TGTTTGGGATGCGAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 005	(65)	TGTTTGGGATGCGAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 006	(65)	TGTTTGGGATGCGAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 007	(65)	TGTTTGGGATGCGAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 008	(65)	TGTTTGGGATGCGAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 009	(65)	TGTTTGGGATGCGAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 010	(65)	TGTTTGGGATGCGAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 011	(75)	CTTCATCCAGCCGAAAGAGCCAAA-GCGGCT	GAGCATAATCCGGTTGTAATGTTGCAT-GGCATGGGTGGTGCG
SEQ: 012	(75)	CTTCATCCAGCCGAAAGAGATCAGA-GCGGCT	GAGCATAATCCGGTTGTTATGTTGCAT-GGCATGGGTGGTGCG
SEQ: 013	(75)	GTTTATCCAGCCGAAAGAGGCGAAG-GCGGCT	GAGCATAATCCGGTTGTTATGTTGCAT-GGCATGGGTGGTGCG
SEQ: 014	(65)	TGTTTGGGATGCGAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 015	(65)	TGTTTGGGATGCGAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 016	(65)	TGTTTGGGATGCGAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 017	(65)	TGTTTGGGATGCGAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 018	(65)	TGTTTGGGATGCGAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT
SEQ: 019	(75)	CTTCATCCAGCCGAAAGAAATCAAA-GCAGCT	GAGCACAATCCGGTTGTTATGTTGCAT-GGTATCGGAGGAGCT
SEQ: 020	(65)	TGTTTGGGATGCGAGCCGTCAGCAAAAGCCGCT	GAACACAATCCAGTTGTTATGTTTCAC-GGTATCGGAGGAGCT

FIGURE 3b



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SEQ: 001	(139)	TCATACAAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAAGGGCAAGCTGTATGCGGTTGAT
SEQ: 002	(139)	TCATTCAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAAGGGCAAGCTGTATGCGGTTGAT
SEQ: 003	(139)	TCATACAAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAAGGGCAAGCTGTATGCGGTTGAT
SEQ: 004	(139)	TCATACAAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAAGGGCAAGCTGTATGCGGTTGAT
SEQ: 005	(139)	TCATACAAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAAGGGCAAGCTGTATGCGGTTGAT
SEQ: 006	(139)	TCATACAAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAAGGGCAAGCTGTATGCGGTTGAT
SEQ: 007	(139)	TCATACAAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAAGGGCAAGCTGTATGCGGTTGAT
SEQ: 008	(139)	TCATACAAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAAGGGCAAGCTGTATGCGGTTGAT
SEQ: 009	(139)	TCATTCAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAAGGGCAAGCTGTATGCGGTTGAT
SEQ: 010	(139)	TCATTCAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAAGGGCAAGCTGTATGCGGTTGAT
SEQ: 011	(148)	TCTTATAACTTTTGGCTTCGATCAAAACGATACTTAGTATCACAGGGATGGGATCAAAACCAACTTTTTCGAATCGAT
SEQ: 012	(148)	TCTTATAACTTTTGGCTTCGATCAAAACGATACTTAGTATCACAGGGATGGGATCAAAACCAACTTTTTCGAATCGAT
SEQ: 013	(148)	TCTTATAACTTTTGGCTTCGATCAAAACGATACTTAGTATCACAGGGATGGGATCAAAACCAACTTTTTCGAATCGAT
SEQ: 014	(139)	TCATTCAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAAGGGCAAGCTGTATGCGGTTGAT
SEQ: 015	(139)	TCATTCAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAAGGGCAAGCTGTATGCGGTTGAT
SEQ: 016	(139)	TCATTCAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAAGGGCAAGCTGTATGCGGTTGAT
SEQ: 017	(139)	TCATTCAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAAGGGCAAGCTGTATGCGGTTGAT
SEQ: 018	(139)	TCATTCAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAAGGGCAAGCTGTATGCGGTTGAT
SEQ: 019	(148)	TCTTATAACTTTTGGCTTCGATCAAAACGATACTTAGTATCACAGGGATGGGATCAAAACCAACTTTTTCGAATCGAT
SEQ: 020	(139)	TCATTCAATTTTGGGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCAAGGGCAAGCTGTATGCGGTTGAT

FIGURE 3c



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226 300

SEQ: 001	(214)	TTTGGGACAAGACAGGACGAATTATAACAATGCCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAA
SEQ: 002	(214)	TTTGGGACAAGACAGGACGAATAATAACAATGGACCGGTATTACCACGATTGTGCAAAAGGTTTAGATGAA
SEQ: 003	(214)	TTTGGGACAAGACAGGACGAATTATAACAATGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAA
SEQ: 004	(214)	TTTGGGACAAGACAGGACGAATTATAACAATGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAA
SEQ: 005	(214)	TTTGGGACAAGACAGGACGAATTATAACAATGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAA
SEQ: 006	(214)	TTTGGGACAAGACAGGACGAATTATAACAATGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAA
SEQ: 007	(214)	TTTGGGACAAGACAGGACGAATTATAACAATGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAA
SEQ: 008	(214)	TTTGGGACAAGACAGGACGAATTATAACAATGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAA
SEQ: 009	(214)	TTCAAGGACAAGACAGGACGAATAATAACAATGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGATGAA
SEQ: 010	(214)	TTCTAAGACAACAAGGGAATAACCGCAACAATGGTCCCGGTATTATCGAGATTCTGCAAAAGATGTGTAGACAAA
SEQ: 011	(223)	TTCTAGACAACAACAGGCAATAACCTAAACAATGGCCCGAGGCTCTCGAGATTCTGTGAAAGACGTAGCCAAA
SEQ: 012	(223)	TTCTAGACAACAACAGGTAATAACCGCAACAATGGTCCCGGTATTATCGAGATTCTGTGCAAAAGATGTGTAGCCAAA
SEQ: 013	(223)	TTCTAGACAACAACAGGAATAACCGCAACAATGGTCCCGGTATTATCGAGATTCTGTGCAAAAGATGTGTAGACAAA
SEQ: 014	(214)	TTCAAGGACAAGACAGGCAATAACTTAAACAACGGTCCAGTATTATCGCGTTTCTGTGAAAGATGTAGATGAA
SEQ: 015	(214)	TTCTGGGATAAGACAGGCAATAACTTAAACAACGGTCCAGTATTATCGCGTTTCTGTGAAAGATGTAGATGAA
SEQ: 016	(214)	TTTAGTGACAACAACAGGCAATAACTTAAACAACGGTCCAGTATTATCGCGTTTCTGTGAAAGATGTAGATGAA
SEQ: 017	(214)	TTCAAGACAAGACAGGGAATAACCGCAACAATGGTCCCGGTATTATCGAGATTCTGTGCAAAAGATGTGTAGACAAA
SEQ: 018	(214)	TTCAATTGACAAGACAGGAATAACCGCAACAATGGTCCCGGTATTATCGAGATTCTGTGCAAAAGATGTGTAGACAAA
SEQ: 019	(223)	TTCTAGACAACAACAGGGAATAACCGCAACAATGGTCCCGTTTATCTAGATTCTGTGCAAAAGATGTGTAGACAAA
SEQ: 020	(214)	TTCAAGGACAAGACAGGAATAACCGCAACAATGGTCCCGGTCTATCTAAATCTGTGCAAAAGATGTGTAGACAAA

FIGURE 3d

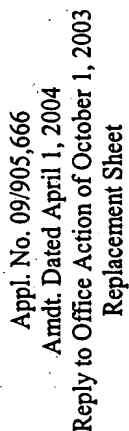


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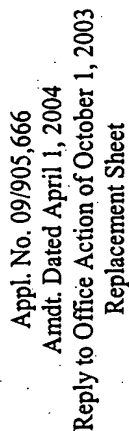
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SEQ: 001 (289) ACGGTGCGAAAAAAGTGATATTGTCGCTCACAGTATGGTGGCGGGAACACACCTTACTACATAAAAAATCTG  
SEQ: 002 (289) ACGGTGCGAAAAAAGTGATATTGTCGCTCACAGCATGGGGGCGGGAACACACCTTACTACATAAAAAATCTG  
SEQ: 003 (289) ACGGTGCGAAAAAAGTGATATTGTCGCTCACAGCATGGGTGGCGGGAACACACCTTACTACATAAAAAATCTG  
SEQ: 004 (289) ACGGTGCGAAAAAAGTGATATTGTCGCTCACAGCATGGGTGGCGGGAACACACCTTACTACATAAAAAATCTG  
SEQ: 005 (289) ACGGTGCGAAAAAAGTGATATTGTCGCTCACAGCATGGGTGGCGGGAACACACCTTACTACATAAAAAATCTG  
SEQ: 006 (289) ACGGTGCGAAAAAAGTGATATTGTCGCTCACAGCATGGGTGGCGGGAACACACCTTACTACATAAAAAATCTG  
SEQ: 007 (289) ACGGTGCGAAAAAAGTGATATTGTCGCTCACAGCATGGGTGGCGGGAACACACCTTACTACATAAAAAATCTG  
SEQ: 008 (289) ACGGTGCGAAAAAAGTGATATTGTCGCTCACAGCATGGGTGGCGGGAACACACCTTACTACATAAAAAATCTG  
SEQ: 009 (289) ACGGTGCGAAAAAAGTGATATTGTCGCTCACAGCATGGGGGCGGGAACACACCTTACTACATAAAAAATCTG  
SEQ: 010 (289) ACGGTGCCAAAAAAGTAGATATTGTGGCTCATAGTATGGGTGGAGCGGAACACGCTATATCAAGAATCTA  
SEQ: 011 (298) ACGGGCGCCAAAAAAGTAGATATTGTGGCTCATAGTATGGCGGTGCGAACACGCTTATAATAAACCTA  
SEQ: 012 (298) ACAGGTGCCAAAAAAGTTGATATTGTGGCTCATAGTATGGCGGAGCGGAACACGTTATAATAAGAATCTA  
SEQ: 013 (298) ACGGTGCCAAAAAAGTAGATATTGTGGCTCATAGTATGGGTGGAGCGGAACACGCTATATCAAGAATCTA  
SEQ: 014 (289) ACCGGTGCAGAAAAAGTGATATTGTCGCTCACAGCATGGGGGCGGCTAACACGCTTACTACATAAAAAATTTG  
SEQ: 015 (289) ACCGGTGCAGAAAAAAGTGATATTGTCGCTCACAGCATGGGGGCGGCTAACACGCTTACTACATAAAAAATTTG  
SEQ: 016 (289) ACCGGTGCAGAAAAAAGTGATATTGTCGCTCACAGCATGGGGGCGGCTAACACGCTTACTACATAAAAAATTTG  
SEQ: 017 (289) ACAGGAGCCAAAAAAGTAGATATTGTGGCTCATAGTATGGCGGAGCGGAACACATTATAATAAGAATCTA  
SEQ: 018 (289) ACAGGAGCCAAAAAAGTAGATATTGTGGCTCATAGTATGGCGGAGCGGAACACATTATAATAAGAATCTA  
SEQ: 019 (298) ACGGTGCCAAAAAAGTAGATATTGTGGCGCATAGTATGGGGGCGGGAACACGCTATATTAAGAATCTA  
SEQ: 020 (289) ACGGTGCCAAAAAAGTAGATATTGTGGCTCATAGTATGGGGGCGGGAACACGCTATATTAAGAATCTA

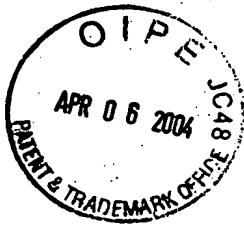
FIGURE 3e



## FIGURE 3f



## FIGURE 3g



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600

SEQ: 001  
SEQ: 002  
SEQ: 003  
SEQ: 004  
SEQ: 005  
SEQ: 006  
SEQ: 007  
SEQ: 008  
SEQ: 009  
SEQ: 010  
SEQ: 011  
SEQ: 012  
SEQ: 013  
SEQ: 014  
SEQ: 015  
SEQ: 016  
SEQ: 017  
SEQ: 018  
SEQ: 019  
SEQ: 020

(513) ATCAAAAATTAGACGGT-GCTAAAAAC-GCTCAAAATTCATGGCGTTGGGCACATTTGGTTATTGATGAACAGCCAA  
(513) ATCAAGATTAGATGGT-GCTAGAAAC-GTTCAAAATCCATGGCGTTGGACACATCGGCCTTCTGTACAGCAGCCAA  
(513) ATCAAAAATTAGACGGT-GCTAAAAAC-GTTCAAAATTCATGGCGTTGGGCACATTTGGTTATTGATGAACAGCCAA  
(513) ATCAAAAATTAGACGGT-GCTAAAAAC-GTTCAAAATTCATGGCGTTGGGCACATTTGGTTATTGATGAACAGCCAA  
(513) ATCAAAAATTAGACGGT-GCTAAAAAC-GTTCAAAATTCATGGCGTTGGGCACATTTGGTTATTGATGAACAGCCAA  
(513) ATCAAAAATTAGACGGT-GCTAAAAAC-GTACAAAATTCATGGCGTTGGGCACATTTGGTTATTGATGAACAGCCAA  
(513) ATCAAAAATTAGACGGT-GCTAAAAAC-GCTCAAAATTCATGGCGTTGGGCACATTTGGTTATTGATGAACAGCCAA  
(513) ATCAAAAATTAGACGGT-GCTAAAAAC-GTTCAAAATTCATGGCGTTGGGCACATTTGGTTATTGATGAACAGCCAA  
(513) ATCAAGATTAGATGGT-GCGAGAAAC-GTTCAAAATCCATGGCGTTGGACACATCGGCCTTCTGTACAGCAGCCAA  
(513) CTCTCGTTTAAATTGGC-GCAAGAAAC-ATCCTGATCCATGGCGTTGGTCATATCGGTCCTATTAACTCAAGCCAA  
(522) TTCGC-GTTTAAATTGGCGCAAGAAAC-GTCTGATCCACGGCGTTGGACATATCGGTCCTATTAACTCAAGCCAA  
(522) CTCGC-GTTTAAATTGGCGCAAGAAAC-GTCTCATTCACGGCGTTGGTCACATCGGTCCTATTAGCTTCAAGCCAA  
(522) CTCTCAGTTTAAATTGGCGCAAGAAAC-ATCCTGATCCA-GGCGTTGGTCATATCGGTCCTATTAACTCAAGCCAA  
(513) AACAAAATTAGACGGG-GCTAAAAAT-GTTCAAAATTCATGGTGTCTGGACATATCGGCCTTCTGTACAGCAGCCAA  
(513) ATCAAAAATTAGACGGG-GCTAAAAAT-GTTCAAAATTCATGGTGTCTGGACATATCGGCCTTCTGTACAGCAGCCAA  
(513) ATCAAAAATTAGACGGG-GCTAAAAAT-GTTCAAAATTCATGGTGTCTGGACATATCGGCCTTCTGTACAGCAGCCAA  
(513) ATCAAAAATTAGACGGG-GCTAAAAAT-GTTCAAAATTCATGGTGTCTGGACATATCGGCCTTCTGTACAGCAGCCAA  
(513) CTCTCGTTTAAATTGGC-GCAAGAAAC-GTCCAAAATCCATGGCGTTGGACATATCGGTCCTATTAACTCAAGCCAA  
(513) CTCTCGTTTAAATTGGC-GCAAGAAAC-GTCCAAAATCCATGGCGTTGGACATATCGGTCCTATTAACTCAAGCCAA  
(522) TTCGC-GTTTAACTGGCGCAAGAAAT-GTCTGATCCACGGCGTTGGCCATATCGGTCCTATTAACTCAAGCCAA  
(514) CTCTCGTTTAAATTGGCTGCAAGAAACAGTCCAAAATCCATGGCGTTGGACATATCGGTCCTATTAACTCAAGCCAA

FIGURE 3h



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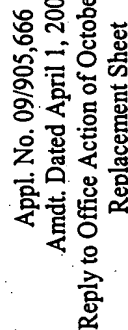
601 654

SEQ: 001 (586) GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGCCAAAATACGAATTAA  
SEQ: 002 (586) GTCAACAGCCTGATTAAAGAGGCTGAACGGCGGGGACTCAATACAAATTAG  
SEQ: 003 (586) GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGCCACAATACAAATTAA  
SEQ: 004 (586) GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGACTAAATACAAATTAA  
SEQ: 005 (586) GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGCTCAATACAAATTAA  
SEQ: 006 (586) GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGCTAGATACAAATTAA  
SEQ: 007 (586) GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGCCACAATACAAATTAA  
SEQ: 008 (586) GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGCCACAATACAAATTAA  
SEQ: 009 (586) GTCAACAGCCTGATTAAAGAGGACTGAACGGCGGGGGCTCAATACAAATTAA  
SEQ: 010 (586) GTGAAAGGGTATTAAAGAGGACTGAACGGCGGGGGCTCAATACAAATTAA  
SEQ: 011 (595) GTCAAGGGCTATGTGAAAGAGGATTGAATGGCGGGGACAGAAATACAAATTAA  
SEQ: 012 (595) GTCAAGGGCTATATCAAGAGGACTGAATGGCGGGAGGCCAAAATACAAATTAA  
SEQ: 013 (595) GTGAAAGGGTATTAAAGAGGACTGAACGGCGGGAGGCCCTCAATACAAATTAA  
SEQ: 014 (586) GTCAACAGCCTGATTAAAGAGGCTTAACGGCGGGAGGCCCTCAATACAAATTAA  
SEQ: 015 (586) GTCAATAGCCTGATTAAAGAGGCTTAACGGCGGGAGGACTCAATACGAATTAA  
SEQ: 016 (586) GTCAACAGCCTGATTAAAGAGGGCTTAACGGCGGGGGCTGAATACGAATTAA  
SEQ: 017 (586) GTCAAGGATATATTAAAGAGGACTGAACGGCGGGGGCTCAATACAAATTAA  
SEQ: 018 (586) GTCAAGGATATATTAAAGAGGACTGAACGGCGGGAGGCCAAAATACAAATTAA  
SEQ: 019 (595) GTGAAAGGGTATTAAAGAGGACTGAACGGCGGGGGCTAAATACAAATTAA  
SEQ: 020 (589) GTCAAGGATATATTAAAGAGGACTGAACGGCGGGGACTAAATACAAATTAA

FIGURE 3i



**FIGURE 4a**



150

**FIGURE4b**



225

151

SEQ: 021 (151) TGGCCCGGTATTATCGCGGTAAGGTAATAGATGAACGGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 022 (151) TGGCCCGGTATTATCTAGATCGTCAAGATGTGCTAGACAAAACGGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 023 (151) TGGCCCGGTATTATCAGCATTTGTGAAAAAGGTAATAGATGAACCGGTGCGAAAAAGTGGACATTTGTCGCTCA  
SEQ: 024 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGACGAAACGGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 025 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGACGAAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 026 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGACGAAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 027 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGACGAAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 028 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGACGAAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 029 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGACGAAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 030 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGACGAAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 031 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGACGAAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 032 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGATGAACCGGTGCGAAAAAGTGGACATTTGTCGCTCA  
SEQ: 033 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGACGAAACCGGTGCGAAAAAGTGGACATTTGTCGCTCA  
SEQ: 034 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGACGAAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 035 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGACGAAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 036 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGATGAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 037 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGATGAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 038 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGATGAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 039 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGATGAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 040 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGACGAAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 041 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGACGAAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 042 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGACGAAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 043 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGACGAAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 044 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGATGAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 045 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGACGAAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 046 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGACGAAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 047 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGATGAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 048 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGATGAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 049 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGATGAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 050 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGATGAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 051 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGATGAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 052 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGACGAAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 053 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGACGAAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA  
SEQ: 054 (151) TGGCCCGGTATTATCAGCATTTGTGCAAAAGGTTTGTAGACGAAACCGGTGCGAAAAAGTGGATATTTGTCGCTCA

FIGURE 4c



226 300

SEQ: 021 (226) CAGCATGGGGCGGCTAACACGCTTTACTACATAAAAAATCTGGACGGCGGAAATAAAGTTGAAAAACGTCGTAAC

SEQ: 022 (226) CAGCATGGGGCGGCGGAACACACTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 023 (226) CAGCATGGGTGGCGGAACACACTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 024 (226) CAGCATGGGGCGGCGGAACACACTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 025 (226) CAGCATGGGGCGGCGGAACACACTTTACTACATAAAAAATCTGGATGGCGGTAATAAATAATTGAAAAACGTCGTCAC

SEQ: 026 (226) CAGCATGGGTGGCGGAACACACTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 027 (226) CAGTATGGGTGGCGGAACACACTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 028 (226) CAGTATGGGTGGCGGAACACACTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 029 (226) CAGCATGGGTGGCGGAACACACTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 030 (226) CAGCATGGGTGGCGGAACACACTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 031 (226) CAGCATGGGTGGCGGAACACACTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 032 (226) CAGCATGGGTGGCGGAACACACTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 033 (226) CAGCATGGGGCGGCTAACACGCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 034 (226) CAGCATGGGGCGGCGGAACACACTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 035 (226) CAGCATGGGTGGCGGGAACACACTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 036 (226) CAGCATGGGTGGCGGGAACACACTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 037 (226) CAGCATGGGTGGCGGGAACACACTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 038 (226) CAGCATGGGTGGCGGGAACACACTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 039 (226) CAGCATGGGTGGCGGGAACACACTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 040 (226) CAGCATGGGGCGGCGGAACACACTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 041 (226) CAGCATGGGGCGGCGGAACACACTTTACTACATAAAAAATCTGGATGGCGGTAATAAATAATTGAAAAACGTCGTAAC

SEQ: 042 (226) CAGCATGGGGCGGCGGAACACACTTTACTACATAAAAAATCTGGACGGCGGTAATAAATAATTGAAAAACGTCGTAAC

SEQ: 043 (226) CAGCATGGGTGGCGGGAACACACTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 044 (226) CAGCATGGGGCGGCGGAACACACTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 045 (226) CAGCATGGGGCGGCGGAACACACTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 046 (226) CAGCATGGGTGGCGGGAACACACTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 047 (226) CAGCATGGGGCGGCGTAACACGCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 048 (226) CAGCATGGGTGGCGGTAACACGCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 049 (226) CAGCATGGGGCGGCGGAACACACTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 050 (226) CAGCATGGGGCGGCGTAACACGCTTTACTACATAAAAAATCTGGATGGCGGTAATAAATAATTGAAAAACGTCGTAAC

SEQ: 051 (226) CAGCATGGGGCGGCGTAACACGCTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 052 (226) CAGCATGGGTGGCGGGAACACACTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 053 (226) CAGCATGGGTGGCGGGAACACACTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

SEQ: 054 (226) CAGCATGGGTGGCGGGAACACACTTTACTACATAAAAAATCTGGACGGCGGAAATAAATAATTGAAAAACGTCGTAAC

FIGURE 4d



301 375

SEQ: 021 (301) GCTTGGCGGCGGACGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 022 (301) GCTTGGCGGCGGACGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 023 (301) GCTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 024 (301) GCTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 025 (301) CATTTGGTGGAGCAAAACGGACTCGTTTCAAGCAGAGCATTTACCAGGACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 026 (301) GCTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 027 (301) GCTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 028 (301) GCTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 029 (301) GCTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 030 (301) GCTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 031 (301) GCTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 032 (301) GCTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 033 (301) GCTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 034 (301) GCTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 035 (301) ACTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 036 (301) GCTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 037 (301) GCTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 038 (301) GCTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 039 (301) GCTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 040 (301) GCTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 041 (301) ACTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 042 (301) ACTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 043 (301) GCTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 044 (301) ACTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 045 (301) ACTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 046 (301) GCTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 047 (301) GCTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 048 (301) GCTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 049 (301) ACTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 050 (301) ACTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 051 (301) GCTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 052 (301) GCTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 053 (301) ACTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC  
SEQ: 054 (301) ACTTGGCGGCGGACGCGTTCGACGACAAAGCGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACAC

FIGURE 4e



376 450

SEQ: 021 (376) ATCCATTACAGCAGTGCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 022 (376) ATCCATTACAGCAGTGCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 023 (376) ATCCATTACAGCAGTGCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 024 (376) ATCCATTACAGCAGTGCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 025 (376) ATCCGTCATAGCTCAGCAGATCTTATTGTCGTCACAGTCTCTCTGTTTAAATGTCGCAAGAAACGTCACAAAT

SEQ: 026 (376) ATCCATTACAGCAGTGCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 027 (376) ATCCGTTTACAGTAGTGCTGATATGATTGTTTATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 028 (376) ATCCGTTTACAGTAGTGCTGATATGATTGTTTATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 029 (376) ATCCGTTTACAGTAGTGCTGATATGATTGTTTATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 030 (376) ATCCGTTTACAGTAGTGCTGATATGATTGTTTATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 031 (376) ATCCGTTTACAGTAGTGCTGATATGATTGTTTATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 032 (376) ATCCATTACAGCAGTGCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 033 (376) ATCCATTACAGCAGTGCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 034 (376) ATCCATTACAGCAGTGCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 035 (376) ATCCATTACAGCAGTGCCGATATGA;TGTCATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 036 (376) ATCCGTTTACAGCAGTGCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 037 (376) ATCCGTTTACAGCAGTGCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 038 (376) ATCCGTTTACAGCAGTGCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 039 (376) ATCCGTTTACAGCAGTGCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 040 (376) ATCCATTACAGCAGTGCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 041 (376) ATCCATTACAGCAGTGCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 042 (376) ATCCATTACAGCAGTGCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 043 (376) ATCCATTACAGCAGTGCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 044 (376) ATCCATTACAGCAGTGCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 045 (376) ATCCATTACAGCAGTGCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 046 (376) ATCCATTACAGCAGTGCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 047 (376) ATCCGTTTACAGTAGTGCTGATATGATTGTTTATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 048 (376) ATCCGTTTACAGTAGTGCTGATATGATTGTTTATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 049 (376) ATCCATTACAGCAGTGCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 050 (376) ATCCATTACAGCAGTGCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 051 (376) ATCCATTACAGCAGTGCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 052 (376) ATCCATTACAGCAGTGCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 053 (376) ATCCATTACAGCAGTGCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

SEQ: 054 (376) ATCCATTACAGCAGTGCCGATATGATTGTCATGAATTAATCTATCAAAATTAAGACGGTGCTAAAAATGTTCAAAT

FIGURE 4f



525  
451  
SEQ: 021 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 022 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 023 (451) CCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 024 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 025 (451) CCATGGCGTTGGGCACATATCGGCTCTAATCACTCAAGCCCAAGTCAAGGATATATTAAAGAGGCTTAAACGGCGG  
SEQ: 026 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAAGGATATATTAAAGAGGACTGAACGGCGG  
SEQ: 027 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAAGGATATATTAAAGAGGACTGAACGGCGG  
SEQ: 028 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAAGGATATATTAAAGAGGACTGAACGGCGG  
SEQ: 029 (451) TCATGGTGTGGGCACATATCGGCTCTGTACAGCAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 030 (451) TCATGGCGTTGGGCACATCGGTTTATTGATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 031 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 032 (451) CCATGGCGTTGGGCACATATCGGCTCTGTACAGCAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 033 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 034 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 035 (451) TCATGGCGTGGGCACATATCGGCTCTGTATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 036 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 037 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 038 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 039 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 040 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 041 (451) TCATGGTGTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 042 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 043 (451) CCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 044 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 045 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 046 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 047 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 048 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 049 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 050 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 051 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 052 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 053 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG  
SEQ: 054 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCCAAGTCAACAGCCTGATTAAGAGGACTGAACGGCGG

FIGURE 4g



	526	544
SEQ: 021	(526)	GGGACTCAATACGAATTGA
SEQ: 022	(526)	GGGACTCAATACGAATTGA
SEQ: 023	(526)	GGGACTGAATACAAAATTGA
SEQ: 024	(526)	GGGACTCAATACGAATTGA
SEQ: 025	(526)	GGGCCACAATACGAATTGA
SEQ: 026	(526)	AGGCCTAAATACGAATTGA
SEQ: 027	(526)	GGGCCTAAATACAAAATTGA
SEQ: 028	(526)	GGGCCTAAATACAAAATTGA
SEQ: 029	(526)	GGGCCAAAAATACAAAATTGA
SEQ: 030	(526)	GGGCCACAATACAAAATTGA
SEQ: 031	(526)	GGGCCTGAATACAAAATTGA
SEQ: 032	(526)	GGGCCTCAATACGAATTGA
SEQ: 033	(526)	GGGACTCAATACGAATTGA
SEQ: 034	(526)	GGGACTCAATACGAATTGA
SEQ: 035	(526)	GGGCCACAATACAAAATTGA
SEQ: 036	(526)	AGGCCACAATACAAAATTGA
SEQ: 037	(526)	AGGCCACAATACAAAATTGA
SEQ: 038	(526)	AGGCCACAATACAAAATTGA
SEQ: 039	(526)	AGGCCACAATACAAAATTGA
SEQ: 040	(526)	GGGCCACAATACAAAATTGA
SEQ: 041	(526)	GGGCCACAATACGAATTGA
SEQ: 042	(526)	GGGATTAAATACGAATTGA
SEQ: 043	(526)	GGGCCAGAATACGAATTGA
SEQ: 044	(526)	AGGCCAGAATACGAATTGA
SEQ: 045	(526)	GGGCCACAATACGAATTGA
SEQ: 046	(526)	GGGCCAGAATACGAATTGA
SEQ: 047	(526)	AGGCCTAAATACAAAATTGA
SEQ: 048	(526)	AGGCCAGAATACGAATTGA
SEQ: 049	(526)	AGGCCAAAAATACGAATTGA
SEQ: 050	(526)	AGGCCAAAAATACGAATTGA
SEQ: 051	(526)	GGGCCAGAATACGAATTGA
SEQ: 052	(526)	AGGCCAAAAATACGAATTGA
SEQ: 053	(526)	GGGCCAAAAATACAAAATTGA
SEQ: 054	(526)	AGGACAAAAATACAAAATTGA

FIGURE 4h





		(Signal peptide)	(Mature region)	
SEQ: 055	(1)	--MKFVKRRRIIALVTILVLSVTSLSFAMQP-SAKAA	EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	40
SEQ: 056	(1)	--MKFVKRRRIIALVTILVLSVTSLSFALQP-SAKAA	EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 057	(1)	--MKFVKRRRIIALVTILVLSVTSLSFAMQP-SAKAA	DTIQLLWFTGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 058	(1)	--MKFVKRRRIIALVTILVLSVTSLSFAMQP-SAKAA	EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 059	(1)	--MKFVKRRRIIALVTILVLSVTSLSFAMQP-SAKAA	EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 060	(1)	--MKFVKRRRIIALVTILVLSVTSLSFAMQP-SAKAA	EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 061	(1)	--MKFVKRRRIIALVTILVLSVTSLSFAMQP-SAKAA	EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 062	(1)	--MKFVKRRRIIALVTILVLSVTSLSFAMQP-SAKAA	EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 063	(1)	--MKFVKRRRIIALVTILVLSVTSLSFAMQP-SAKAA	EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 064	(1)	--MKFVKRRRIIALVTILVLSVTSLSFALQP-SAKAA	EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 065	(1)	--MKFVKRRRIIALVTILVLSVTSLSFALQP-SAKAA	EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 066	(1)	MKVIFVKRRSLQILVALVLSGSAFIQPKKEAKAA	EHNPVVMVHGMGGASYNFASIKRYLVSQGWDQNQLFAIDF	
SEQ: 067	(1)	MKVIFVKRRSLQILVALVLSGSAFIQPKKEAKAA	EHNPVVMVHGMGGASYNFASIKRYLVSQGWDQNQLFAIDF	
SEQ: 068	(1)	MKVIFVKRRSLQILVALVLSGSAFIQPKKEAKAA	EHNPVVMVHGMGGASYNFASIKRYLVSQGWDQNQLFAIDF	
SEQ: 069	(1)	--MKFVKRRRIIALVTILVLSVTSLSFALQP-SAKAA	EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 070	(1)	--MKFVKRRRIIALVTILVLSVTSLSFALQP-SAKAA	EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 071	(1)	--MKFVKRRRIIALVTILVLSVTSLSFALQP-SAKAA	EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 072	(1)	--MKFVKRRRIIALVTILVLSVTSLSFALQP-SAKAA	EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 073	(1)	--MKFVKRRRIIALVTILVLSVTSLSFALQP-SAKAA	EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 074	(1)	--MKFVKRRRIIALVTILVLSVTSLSFALQP-SAKAA	EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRDKLYAVDF	

FIGURE 5a



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SEQ: 055	(73) WDKTGTNNNGPVL	SRFVQKVL	DETGAKKVD	IVAHSMGGANTL	YIKNLDGGNKI	ENNVVTLGGANRSTTSKALPG
SEQ: 056	(73) WDKTGTNNNGPVL	PRFVQKVL	DETGAKKVD	IVAHSMGGANTL	YIKNLDGGNKI	ENNVVTLGGANRLTTGKALPG
SEQ: 057	(73) WDKTGTNNNGPVL	SRFVQKVL	DETGAKKVD	IVAHSMGGANTL	YIKNLDGGNKI	ENNVVTLGGANRLTTGKALPG
SEQ: 058	(73) WDKTGTNNNGPVL	SRFVQKVL	DETGAKKVD	IVAHSMGGANTL	YIKNLDGGNKI	ENNVVTLGGANRLTTGKALPG
SEQ: 059	(73) WDKTGTNNNGPVL	SRFVQKVL	DETGAKKVD	IVAHSMGGANTL	YIKNLDGGNKI	ENNVVTLGGANRLTTGKALPG
SEQ: 060	(73) WDKTGTNNNGPVL	SRFVQKVL	DETGAKKVD	IVAHSMGGANTL	YIKNLDGGNKI	ENNVVTLGGANRLTTGKALPG
SEQ: 061	(73) WDKTGTNNNGPVL	SRFVQKVL	DETGAKKVD	IVAHSMGGANTL	YIKNLDGGNKI	ENNVVTLGGANRLTTGKALPG
SEQ: 062	(73) WDKTGTNNNGPVL	SRFVQKVL	DETGAKKVD	IVAHSMGGANTL	YIKNLDGGNKI	ENNVVTLGGANRLTTGKALPG
SEQ: 063	(73) KDKTGTNNNGPVL	SRFVQKVL	DETGAKKVD	IVAHSMGGANTL	YIKNLDGGNKI	ENNVVTLGGANRLTTGKALPG
SEQ: 064	(73) XDKTGTNNNGPVL	SRFVQKVL	DETGAKKVD	IVAHSMGGANTL	YIKNLDGGNKI	ENNVVTLGGANRLTTGKALPG
SEQ: 065	(76) IDKTGNNLNGPRL	SRFVKDVL	DKTGAKKVD	IVAHSMGGANTL	YIKNLDGGDKI	ENNVVTLGGANGLVSSRALPG
SEQ: 066	(76) IDKTGNNLNGPRL	SRFVKDVL	AKTGAKKVD	IVAHSMGGANTL	YIKNLDGGDKI	ENNVVTLGGANGLVSLRALPG
SEQ: 067	(76) IDKTGNNRNGPRL	SRFVKDVL	LAKTGAKKVD	IVAHSMGGANTL	YIKNLDGGDKI	ENNVVTLGGANGLVSLRALPG
SEQ: 068	(73) RDKTGNNLNGPVL	SRFVKKVL	DETGAKKVD	IVAHSMGGANTL	YIKNLDGGDKI	ENNVVTLGGANGLVSSRALPG
SEQ: 069	(73) WDKTGNNLNGPVL	SRFVKKVL	DETGAKKVD	IVAHSMGGANTL	YIKNLDGGNKI	ENNVVTLGGANRLVTGKALPG
SEQ: 070	(73) SDKTGNNLNGPVL	SRFVKKVL	DETGAKKVD	IVAHSMGGANTL	YIKNLDGGNKI	ENNVVTLGGANRLVTGKALPG
SEQ: 071	(73) KDKTGNNRNGPRL	SRFVKDVL	DKTGAKKVD	IVAHSMGGANTL	YIKNLDGGDKI	ENNVVTLGGANGLVSSRALPG
SEQ: 072	(73) IDKTGNNRNGPRL	SRFVKDVL	DKTGAKKVD	IVAHSMGGANTL	YIKNLDGGDKI	ENNVVTLGGANGLVSSRALPG
SEQ: 073	(76) IDKTGNNRNGPRL	SRFVKDVL	DKTGAKKVD	IVAHSMGGANTL	YIKNLDGGDKI	ENNVVTLGGANGLVSLRALPG
SEQ: 074	(73) RDKTGNNRNGPRL	SKFVKDVL	DKTGAKKVD	IVAHSMGGANTL	YIKNLDGGDKI	ENNVVTLGGANGLVSSRALPG

FIGURE 5b



116  
SEQ: 055 TDPNQILYTSYSSADMIVMN- YLSKLDGAKNAQIHGVGHI GLLMNSQVNSLIKEGLNGGGQNTN  
SEQ: 056 TDPNQILYTSYSSADMIVN- YLSRLDGARNVQIHGVGHI GLLYSSQVNSLIKEGLNGGGLNTN  
SEQ: 057 TDPNQILYTSYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLMNSQVNSLIKEGLNGGGHNTN  
SEQ: 058 TDPNQILYTSYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLMNSQVNSLIKEGLNGGGLNTN  
SEQ: 059 TDPNQILYTSYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLMNSQVNSLIKEGLNGGGLNTN  
SEQ: 060 TDPNQILYTSYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLMNSQVNSLIKEGLNGGGLDNTN  
SEQ: 061 TDPNQILYTSYSSADMIVMN- YLSKLDGAKNAQIHGVGHI GLLMNSQVNSLIKEGLNGGGHNTN  
SEQ: 062 TDPNQILYTSYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLMNSQVNSLIKEGLNGGGHNTN  
SEQ: 063 TDPNQILYTSYSSADMIVMN- YLSRLDGARNVQIHGVGHI GLLYSSQVNSLIKEGLNGGGLNTN  
SEQ: 064 TDPNQILYTSYSSADLIWN- SLSRLIGARNVLIHGVLIGLLTSSQVKGYIKEGLNGGGLNTN  
SEQ: 065 TDPNQILYTSYSSADLIWN- SLSRLIGARNVLIHGVLIGLLTSSQVKGYIKEGLNGGGQNTN  
SEQ: 066 TDPNQILYTSYSSADLIWN- SLSRLIGARNVLIHGVLIGLLASSQVKGYIKEGLNGGGQNTN  
SEQ: 067 TDPNQILYTSYSSADLIWN- SLSQFNWRKKHPDPGVGHI GLLTSSQVKGYIKEGLNGGGLNTN  
SEQ: 068 TDPNQILYTSYSSADMIVMN- YLTCLDGAKNVQIHGVGHI GLLYSSQVNSLIKEGLNGGGLNTN  
SEQ: 069 TDPNQILYTSYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLYSSQVNSLIKEGLNGGGLNTN  
SEQ: 070 TDPNQILYTSYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLYSSQVNSLIKEGLNGGGLNTN  
SEQ: 071 TDPNQILYTSYSSADLIWN- SLSRLIGARNVQIHGVGHI GLLTSSQVKGYIKEGLNGGGLNTN  
SEQ: 072 TDPNQILYTSYSSADLIWN- SLSRLIGARNVQIHGVGHI GLLTSSQVKGYIKEGLNGGGQNTN  
SEQ: 073 TDPNQILYTSYSSADLIWN- SLSRLTGARNVLIHGVLIGLLTSSQVKGYIKEGLNGGGLNTN  
SEQ: 074 TDPNQILYTSYKLSRSHCRQQLSFNWLQETVQIHGVGHI GLLTSSQVKGYIKEGLNGGGLNTN

FIGURE 5c



1 75

SEQ: 075 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 076 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 077 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 078 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 079 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 080 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 081 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 082 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 083 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 084 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 085 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 086 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 087 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 088 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 089 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 090 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 091 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 092 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 093 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 094 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 095 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 096 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 097 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 098 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 099 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 100 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 101 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 102 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 103 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 104 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 105 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 106 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 107 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

SEQ: 108 (1) EHNPMVHVHIGGASFNAGIKSYLVSQWSRGKLYAVDFWDDKTGTNNNGPVL SRFVKKVLDLDTGAKKKVD IVAH

FIGURE 6a



150  
76  
SEQ: 075 (76) SMGGANTLYYIKNLDGGNKVENVVTGGTNRSTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 076 (76) SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 077 (76) SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 078 (76) SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 079 (76) SMGGANTLYYIKNLDGGNKIENVVTLGGANGLVSSRALPGTDPNQKILYTSYSSADLIVNLSRLIGARNVQI  
SEQ: 080 (76) SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSRALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 081 (76) SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 082 (76) SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 083 (76) SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 084 (76) SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 085 (76) SMGGANTLYYIKNLDGGNKIENVVTLGGANRLVTGKALPGTDPNQKILYASVYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 086 (76) SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 087 (76) SMGGANTLYYIKNLDGGNKIENVVTLGGTNRSTTSRALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 088 (76) SMGGANTLYYIKNLDGGNKVENVVTGGANRLTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 089 (76) SMGGANTLYYIKNLDGGNKVESVVTGGANRLVTGKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 090 (76) SMGGANTLYYIKNLDGGNKVENVVTGGANRLTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 091 (76) SMGGANTLYYIKNLDGGNKVENVVTGGANRLTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 092 (76) SMGGANTLYYIKNLDGGNKVENVVTGGANRLTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 093 (76) SMGGANTLYYIKNLDGGNKVENVVTGGANRLTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 094 (76) SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 095 (76) SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 096 (76) SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 097 (76) SMGGANTLYYIKNLDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 098 (76) SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 099 (76) SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 100 (76) SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 101 (76) SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 102 (76) SMGGANTLYYIKNLDGGDKIENVVTLGGANRSTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 103 (76) SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 104 (76) SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 105 (76) SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 106 (76) SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 107 (76) SMGGANTLYYIKNLDGGNKVENVVTGGANRSTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI  
SEQ: 108 (76) SMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSYSSADMIVMNYLSKLDGAKNVQI

FIGURE 6b



151  
SEQ: 075 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN  
SEQ: 076 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN  
SEQ: 077 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN  
SEQ: 078 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN  
SEQ: 079 (151) HGVGHIGLLTSSQVKGVIKEGLNGGGHNTN  
SEQ: 080 (151) HGVGHIGLLMNSQVKGVIKEGLNGGGLNTN  
SEQ: 081 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN  
SEQ: 082 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN  
SEQ: 083 (151) HGVGHIGLLYSSQVNSLIKEGLNGGGQNTN  
SEQ: 084 (151) HGVGHTGLMNSQVNSLIKEGLNGGGHNTN  
SEQ: 085 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN  
SEQ: 086 (151) HGVGHIGLLYSSQVNSLIKEGLNGGGLNTN  
SEQ: 087 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN  
SEQ: 088 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN  
SEQ: 089 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGHNTN  
SEQ: 090 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGHNTN  
SEQ: 091 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGHNTN  
SEQ: 092 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGHNTN  
SEQ: 093 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGHNTN  
SEQ: 094 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGHNTN  
SEQ: 095 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGHNTN  
SEQ: 096 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGHNTN  
SEQ: 097 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN  
SEQ: 098 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGQNTN  
SEQ: 099 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGQNTN  
SEQ: 100 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGHNTN  
SEQ: 101 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGQNTN  
SEQ: 102 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN  
SEQ: 103 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGQNTN  
SEQ: 104 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGQNTN  
SEQ: 105 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGQNTN  
SEQ: 106 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGQNTN  
SEQ: 107 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGQNTN  
SEQ: 108 (151) HGVGHIGLLMNSQVNSLIKEGLNGGGQNTN  
180

FIGURE 6c